

SEQUENCE LISTING

<110> Tao, Yumin
Gordon-Kamm William J.
Lowe, Keith S.
Bailey, Matthew A.

<120> Cell Cycle Polynucleotide, Polypeptide,
and Uses Thereof

<130> 1109

<150> US 60/119,857
<151> 1999-02-12

<150> US 60/101,551
<151> 1998-09-23

<150> US 09/398,858
<151> 1999-09-20

<150> US 09/257,131
<151> 1999-02-25

<160> 8

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 1636
<212> DNA
<213> Zea mays

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<221> CDS
<222> (109) ... (1381)

<221> misc_feature
<222> (1) ... (1636)
<223> n = A, T, C or G

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tcacggggct cctccgtccg taaggcacccg ccgcagcgtc tcggctggat caacaggccg
gcccgcgtt cttttccccc tcctcctgcg ggtcggcggt tggggatc atg gcg gcg
Met Ala Ala
1

cg gct gac gag aac agg aga ccg gcg gca ggg aag ccc gcg cca
Arg Ala Ala Asp Glu Asn Arg Arg Pro Ala Ala Gly Lys Pro Ala Pro
5 10 15
165

ggc gtc cga gac atg gcg agc ccg cgc gcg ctc acg gac atc aag aac
Gly Val Arg Asp Met Ala Ser Arg Arg Ala Leu Thr Asp Ile Lys Asn
20 25 30 35
213

ctc gtc ggg gct gcc ccg tac ccc tac gcc gtc gcc aag aag ccc atg
Leu Val Gly Ala Ala Pro Tyr Pro Tyr Ala Val Ala Lys Lys Pro Met
40 45 50
261

ctg cag aag agc aaa agg gac gaa aag cag cca gcg ttg gca agc agc
Leu Gln Lys Ser Lys Arg Asp Glu Lys Gln Pro Ala Leu Ala Ser Ser
309

55

60

65

cg g ccc atg aca agg aaa ttc gcc gcc tcc ttg gcg agc aag ggc caa Arg Pro Met Thr Arg Lys Phe Ala Ala Ser Leu Ala Ser Lys Gly Gln	357
70 75 80	
cct gaa tgt cag cc g atc gta gct gat cca gaa ccc gaa gtt tgt caa Pro Glu Cys Gln Pro Ile Val Ala Asp Pro Glu Pro Glu Val Cys Gln	405
85 90 95	
cag aag gaa tca gta ggc gat ggc acc gtt gat att gac gtg gaa ctc Gln Lys Glu Ser Val Gly Asp Gly Thr Val Asp Ile Asp Val Glu Leu	453
100 105 110 115	
tac gag ctg gtc gac ggt agt gat agt gac atc gac atg ggt gcg aca Tyr Glu Leu Val Asp Gly Ser Asp Ser Asp Ile Asp Met Gly Ala Thr	501
120 125 130	
gag aac aag gac att atg aac gaa gat gaa ttg ctc atg gat att gac Glu Asn Lys Asp Ile Met Asn Glu Asp Glu Leu Leu Met Asp Ile Asp	549
135 140 145	
agt gca gac tcg ggg aac cc g ctt gct gca aca gaa tat gtt aaa gag Ser Ala Asp Ser Gly Asn Pro Leu Ala Ala Thr Glu Tyr Val Lys Glu	597
150 155 160	
ctt tac acc ttt tac aga gaa aat gag gct aag agt tgt gta agg cca Leu Tyr Thr Phe Tyr Arg Glu Asn Glu Ala Lys Ser Cys Val Arg Pro	645
165 170 175	
gat tac atg tcc agc caa caa gac ata aac tca aag atg aga gca att Asp Tyr Met Ser Ser Gln Gln Asp Ile Asn Ser Lys Met Arg Ala Ile	693
180 185 190 195	
ctg att gac tgg ctg att gag gtt cac tac aag ttt gaa ctg atg gat Leu Ile Asp Trp Leu Ile Glu Val His Tyr Lys Phe Glu Leu Met Asp	741
200 205 210	
gag acg ctc ttt ctt atg gta aac ata ata gat aga ttc ttg gaa aag Glu Thr Leu Phe Leu Met Val Asn Ile Ile Asp Arg Phe Leu Glu Lys	789
215 220 225	
gaa gtg gtt cca agg aag aag cta caa ctg gtt gga gtc aca gct atg Glu Val Val Pro Arg Lys Lys Leu Gln Leu Val Gly Val Thr Ala Met	837
230 235 240	
ctg ctc gct tgt aaa tat gag gag gta tct gtt cca gtt gtt gag gac Leu Leu Ala Cys Lys Tyr Glu Glu Val Ser Val Pro Val Val Glu Asp	885
245 250 255	
ctt gtg ctg ata tct gac cgt gcc tac aca aaa ggg caa att tta gaa Leu Val Leu Ile Ser Asp Arg Ala Tyr Thr Lys Gly Gln Ile Leu Glu	933
260 265 270 275	
atg gaa aag ttg att ctg aac acg ctg cag ttc aac atg tct gtt cca Met Glu Lys Leu Ile Leu Asn Thr Leu Gln Phe Asn Met Ser Val Pro	981
280 285 290	
aca cct tat gtc ttc atg aag agg ttt ctg aaa gct gca gat gca gat Thr Pro Tyr Val Phe Met Lys Arg Phe Leu Lys Ala Ala Asp Ala Asp	1029
295 300 305	

aaa cag ctt gag cta gcg tca ttt ttc atg ctg gag ctc tgc ttg gta 1077
 Lys Gln Leu Glu Leu Ala Ser Phe Phe Met Leu Glu Leu Cys Leu Val
 310 315 320

 gaa tac caa atg ctg aat tat cgg cct tcg cat ctg gct gct gct gcg 1125
 Glu Tyr Gln Met Leu Asn Tyr Arg Pro Ser His Leu Ala Ala Ala Ala
 325 330 335

 gtt tat act gca cag tgt gct atc aat cgt tgc cag cac tgg aca aag 1173
 Val Tyr Thr Ala Gln Cys Ala Ile Asn Arg Cys Gln His Trp Thr Lys
 340 345 350 355

 gtc tgc gag tct cat agc aga tac act agc gac caa ctc ctg gag tgc 1221
 Val Cys Glu Ser His Ser Arg Tyr Thr Ser Asp Gln Leu Leu Glu Cys
 360 365 370

 tcg agg atg atg gta gat ttt cac cag aag gct gga acc agt aag ctc 1269
 Ser Arg Met Met Val Asp Phe His Gln Lys Ala Gly Thr Ser Lys Leu
 375 380 385

 act ggc gtg cac agg aag tac agt acc tac aag ttc ggt tgc gtg gcc 1317
 Thr Gly Val His Arg Lys Tyr Ser Thr Tyr Lys Phe Gly Cys Val Ala
 390 395 400

 aag att ttg cct gcg cag ttc ctg ctg gag tcg gga ggg aca cca cct 1365
 Lys Ile Leu Pro Ala Gln Phe Leu Leu Glu Ser Gly Gly Thr Pro Pro
 405 410 415

 cct tca ggt gca aac t agttgaatcg acctattcaa ctgggtggat tttttaaagt 1421
 Pro Ser Gly Ala Asn
 420

 ttttagaata ctccatgaac aagatgcaga aaacatcgta ttgatgttgc ccaaaagtgc 1481
 atcgaatttc ttggagagt tatgattaac aactttttt ttatctatgt tgaatgacga 1541
 gtgacggctcg gtcacgttgt gcttgtcag ttatactgcg gctaataaca aactgtccag 1601
 ttnttctnaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaa 1636

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 <211> 424
 <212> PRT
 <213> Zea mays

 <400> 2
 Met Ala Ala Arg Ala Ala Asp Glu Asn Arg Arg Pro Ala Ala Gly Lys
 1 5 10 15
 Pro Ala Pro Gly Val Arg Asp Met Ala Ser Arg Arg Ala Leu Thr Asp
 20 25 30
 Ile Lys Asn Leu Val Gly Ala Ala Pro Tyr Pro Tyr Ala Val Ala Lys
 35 40 45
 Lys Pro Met Leu Gln Lys Ser Lys Arg Asp Glu Lys Gln Pro Ala Leu
 50 55 60
 Ala Ser Ser Arg Pro Met Thr Arg Lys Phe Ala Ala Ser Leu Ala Ser
 65 70 75 80
 Lys Gly Gln Pro Glu Cys Gln Pro Ile Val Ala Asp Pro Glu Pro Glu
 85 90 95
 Val Cys Gln Gln Lys Glu Ser Val Gly Asp Gly Thr Val Asp Ile Asp
 100 105 110
 Val Glu Leu Tyr Glu Leu Val Asp Gly Ser Asp Ser Asp Ile Asp Met
 115 120 125
 Gly Ala Thr Glu Asn Lys Asp Ile Met Asn Glu Asp Glu Leu Leu Met
 130 135 140
 Asp Ile Asp Ser Ala Asp Ser Gly Asn Pro Leu Ala Ala Thr Glu Tyr

145	150	155	160
Val Lys Glu Leu Tyr Thr Phe Tyr Arg Glu Asn Glu Ala Lys Ser Cys			
165	170	175	
Val Arg Pro Asp Tyr Met Ser Ser Gln Gln Asp Ile Asn Ser Lys Met			
180	185	190	
Arg Ala Ile Leu Ile Asp Trp Leu Ile Glu Val His Tyr Lys Phe Glu			
195	200	205	
Leu Met Asp Glu Thr Leu Phe Leu Met Val Asn Ile Ile Asp Arg Phe			
210	215	220	
Leu Glu Lys Glu Val Val Pro Arg Lys Lys Leu Gln Leu Val Gly Val			
225	230	235	240
Thr Ala Met Leu Leu Ala Cys Lys Tyr Glu Glu Val Ser Val Pro Val			
245	250	255	
Val Glu Asp Leu Val Leu Ile Ser Asp Arg Ala Tyr Thr Lys Gly Gln			
260	265	270	
Ile Leu Glu Met Glu Lys Leu Ile Leu Asn Thr Leu Gln Phe Asn Met			
275	280	285	
Ser Val Pro Thr Pro Tyr Val Phe Met Lys Arg Phe Leu Lys Ala Ala			
290	295	300	
Asp Ala Asp Lys Gln Leu Glu Leu Ala Ser Phe Phe Met Leu Glu Leu			
305	310	315	320
Cys Leu Val Glu Tyr Gln Met Leu Asn Tyr Arg Pro Ser His Leu Ala			
325	330	335	
Ala Ala Ala Val Tyr Thr Ala Gln Cys Ala Ile Asn Arg Cys Gln His			
340	345	350	
Trp Thr Lys Val Cys Glu Ser His Ser Arg Tyr Thr Ser Asp Gln Leu			
355	360	365	
Leu Glu Cys Ser Arg Met Met Val Asp Phe His Gln Lys Ala Gly Thr			
370	375	380	
Ser Lys Leu Thr Gly Val His Arg Lys Tyr Ser Thr Tyr Lys Phe Gly			
385	390	395	400
Cys Val Ala Lys Ile Leu Pro Ala Gln Phe Leu Leu Glu Ser Gly Gly			
405	410	415	
Thr Pro Pro Pro Ser Gly Ala Asn			
420			

<210> 3
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> primer_bind
 <222> (1)...(21)

<400> 3
 ctagttgca cctgaaggag g
 21

<210> 4
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
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 <222> (1)...(22)

<400> 4
 gctaagagtt gtgttaaggcc ag
 22

<210> 5
<211> 21
<212> DNA
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<220>
<221> primer_bind
<222> (1)...(21)

<400> 5
ttggccaaca tcaacacgat g
21

<210> 6
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<222> (1)...(23)

<400> 6
aacccgccttg ctgcaacaga ata
23

<210> 7
<211> 23
<212> DNA
<213> artificial organism

<220>
<221> primer_bind
<222> (1)...(23)

<400> 7
aatccaccca gttgaatagg tcg
23

<210> 8
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<222> (1)...(23)

<400> 8
atccgttcc ttccccctcct cct
23